



# SEQUENCE LISTING

<110> GOOD, Allen G.  
STROEHER, Virginia L.  
MUENCH, Douglas G.

<120> PLANTS WITH ENHANCED LEVELS OF NITROGEN  
UTILIZATION PROTEINS IN THEIR ROOT EPIDERMIS AND USES  
THEREOF

<130> 595792000420

<140> 10/756,213

<141> 2004-01-12

<150> 10/321,718

<151> 2002-12-17

<150> 09/493,803

<151> 2000-01-28

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 365

<212> DNA

<213> Brassica napus

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aacagctcag ctttcgtttt cgggtccaatc gctgttccaa ctttacttac aagtcgtaca 180
cgtctctctc tctctctctc tctctcactc acttctctct ataaagactc tctgatcaaa 240
cgtataatcg gaaaactcca ttctttgata ccacgcataa tactaagaga ggtgattgat 300
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<212> DNA

<213> Barley

<220>

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Met Ala Ala Thr Val Ala Val
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1

5

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Asp Asn Leu Asn Pro Lys Val Leu Lys Cys Glu Tyr Ala Val Arg Gly
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10	15	20	
gag att gtc atc cat gct cag cgc ttg cag gaa cag cta aag act caa			211
Glu Ile Val Ile His Ala Gln Arg Leu Gln Glu Gln Leu Lys Thr Gln			
25	30	35	
cca ggg tct cta cct ttt gat gag atc ctc tat tgt aac att ggg aac			259
Pro Gly Ser Leu Pro Phe Asp Glu Ile Leu Tyr Cys Asn Ile Gly Asn			
40	45	50	55
cca caa tct ctt ggt cag caa cca gtt aca ttc ttc agg gag gtt ctt			307
Pro Gln Ser Leu Gly Gln Gln Pro Val Thr Phe Phe Arg Glu Val Leu			
60	65	70	
gcc ctt tgt gat cat cca gac ctg ttg caa aga gag gaa atc aaa aca			355
Ala Leu Cys Asp His Pro Asp Leu Leu Gln Arg Glu Glu Ile Lys Thr			
75	80	85	
ttg ttc agt gct gat tct att tct cga gca aag cag att ctt gcc atg			403
Leu Phe Ser Ala Asp Ser Ile Ser Arg Ala Lys Gln Ile Leu Ala Met			
90	95	100	
ata cct gga aga gca aca gga gca tac agc cat agc cag ggt att aaa			451
Ile Pro Gly Arg Ala Thr Gly Ala Tyr Ser His Ser Gln Gly Ile Lys			
105	110	115	
gga ctt cgt gat gca att gct tct ggg atc gct tca cga gat gga ttc			499
Gly Leu Arg Asp Ala Ile Ala Ser Gly Ile Ala Ser Arg Asp Gly Phe			
120	125	130	135
cct gct aat gct gat gac att ttt ctc aca gat gga gca agt cct ggg			547
Pro Ala Asn Ala Asp Asp Ile Phe Leu Thr Asp Gly Ala Ser Pro Gly			
140	145	150	
gtg cac ctg atg atg caa tta ctg ata agg aat gag aaa gat ggc att			595
Val His Leu Met Met Gln Leu Leu Ile Arg Asn Glu Lys Asp Gly Ile			
155	160	165	
ctt gtc ccg att cct cag tac ccc ttg tac tcg gct tcc ata gct ctt			643
Leu Val Pro Ile Pro Gln Tyr Pro Leu Tyr Ser Ala Ser Ile Ala Leu			
170	175	180	
cat ggc gga gct ctt gtc cca tac tat ctc aat gaa tcg acg ggc tgg			691
His Gly Gly Ala Leu Val Pro Tyr Tyr Leu Asn Glu Ser Thr Gly Trp			
185	190	195	
ggg ttg gaa acc tct gat gtt aag aag caa ctt gaa gat gct cgg tca			739
Gly Leu Glu Thr Ser Asp Val Lys Lys Gln Leu Glu Asp Ala Arg Ser			
200	205	210	215
aga ggc atc aac gtt agg gct ttg gtg gtt atc aat cca gga aat cca			787
Arg Gly Ile Asn Val Arg Ala Leu Val Val Ile Asn Pro Gly Asn Pro			
220	225	230	
act gga cag gta ctt gct gaa gaa aac caa tat gac ata gtg aag ttc			835
Thr Gly Gln Val Leu Ala Glu Glu Asn Gln Tyr Asp Ile Val Lys Phe			
235	240	245	

tgc aaa aat gag ggt ctt gtt ctt cta gct gat gag gta tac caa gag	883
Cys Lys Asn Glu Gly Leu Val Leu Leu Ala Asp Glu Val Tyr Gln Glu	
250 255 260	
aac atc tat gtt gac aac aag aaa ttc cac tct ttc aag aag ata gtg	931
Asn Ile Tyr Val Asp Asn Lys Lys Phe His Ser Phe Lys Lys Ile Val	
265 270 275	
aga tcc ttg gga tac ggc gag gag gat ctc cct cta gta tca tat caa	979
Arg Ser Leu Gly Tyr Gly Glu Glu Asp Leu Pro Leu Val Ser Tyr Gln	
280 285 290 295	
tct gtt tct aag gga tat tat ggt gag tgt ggt aaa aga ggt ggt tac	1027
Ser Val Ser Lys Gly Tyr Tyr Gly Glu Cys Gly Lys Arg Gly Gly Tyr	
300 305 310	
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Phe Glu Ile Thr Gly Phe Ser Ala Pro Val Arg Glu Gln Ile Tyr Lys	
315 320 325	
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Ile Ala Ser Val Asn Leu Cys Ser Asn Ile Thr Gly Gln Ile Leu Ala	
330 335 340	
agt ctt gtc atg aac cca cca aag gct agt gat gaa tca tac gct tca	1171
Ser Leu Val Met Asn Pro Pro Lys Ala Ser Asp Glu Ser Tyr Ala Ser	
345 350 355	
tac aag gca gaa aaa gat gga atc ctc gca tct tta gct cgt cgt gcg	1219
Tyr Lys Ala Glu Lys Asp Gly Ile Leu Ala Ser Leu Ala Arg Arg Ala	
360 365 370 375	
aag gca ttg gag cat gca ttc aat aaa ctt gag gga att act tgc aac	1267
Lys Ala Leu Glu His Ala Phe Asn Lys Leu Glu Gly Ile Thr Cys Asn	
380 385 390	
gag gct gaa gga gca atg tac gtg ttc cct caa atc tgt ctg cca cag	1315
Glu Ala Glu Gly Ala Met Tyr Val Phe Pro Gln Ile Cys Leu Pro Gln	
395 400 405	
aag gca att gag gct gct aaa gct gct aac aaa gca cct gat gca ttc	1363
Lys Ala Ile Glu Ala Ala Lys Ala Ala Asn Lys Ala Pro Asp Ala Phe	
410 415 420	
tat gct ctt cgt ctc ctc gag tcg act gga atc gtc gtt gtc cct gga	1411
Tyr Ala Leu Arg Leu Leu Glu Ser Thr Gly Ile Val Val Val Pro Gly	
425 430 435	
tca gga ttt ggc cag gtt cct ggc aca tgg cac ttc agg tgc acg atc	1459
Ser Gly Phe Gly Gln Val Pro Gly Thr Trp His Phe Arg Cys Thr Ile	
440 445 450 455	
ctt ccg cag gag gat aag atc ccg gca gtc atc tcc cgc ttc acg gtg	1507
Leu Pro Gln Glu Asp Lys Ile Pro Ala Val Ile Ser Arg Phe Thr Val	
460 465 470	

ttc cat gag gcg ttc atg tca gag tat cgt gac taaactggtg caacatgtgg 1560  
Phe His Glu Ala Phe Met Ser Glu Tyr Arg Asp  
475 480

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<212> PRT  
<213> Barley

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Gln Glu Gln Leu Lys Thr Gln Pro Gly Ser Leu Pro Phe Asp Glu Ile  
35 40 45  
Leu Tyr Cys Asn Ile Gly Asn Pro Gln Ser Leu Gly Gln Gln Pro Val  
50 55 60  
Thr Phe Phe Arg Glu Val Leu Ala Leu Cys Asp His Pro Asp Leu Leu  
65 70 75 80  
Gln Arg Glu Glu Ile Lys Thr Leu Phe Ser Ala Asp Ser Ile Ser Arg  
85 90 95  
Ala Lys Gln Ile Leu Ala Met Ile Pro Gly Arg Ala Thr Gly Ala Tyr  
100 105 110  
Ser His Ser Gln Gly Ile Lys Gly Leu Arg Asp Ala Ile Ala Ser Gly  
115 120 125  
Ile Ala Ser Arg Asp Gly Phe Pro Ala Asn Ala Asp Asp Ile Phe Leu  
130 135 140  
Thr Asp Gly Ala Ser Pro Gly Val His Leu Met Met Gln Leu Leu Ile  
145 150 155 160  
Arg Asn Glu Lys Asp Gly Ile Leu Val Pro Ile Pro Gln Tyr Pro Leu  
165 170 175  
Tyr Ser Ala Ser Ile Ala Leu His Gly Gly Ala Leu Val Pro Tyr Tyr  
180 185 190  
Leu Asn Glu Ser Thr Gly Trp Gly Leu Glu Thr Ser Asp Val Lys Lys  
195 200 205  
Gln Leu Glu Asp Ala Arg Ser Arg Gly Ile Asn Val Arg Ala Leu Val  
210 215 220  
Val Ile Asn Pro Gly Asn Pro Thr Gly Gln Val Leu Ala Glu Glu Asn  
225 230 235 240  
Gln Tyr Asp Ile Val Lys Phe Cys Lys Asn Glu Gly Leu Val Leu Leu  
245 250 255  
Ala Asp Glu Val Tyr Gln Glu Asn Ile Tyr Val Asp Asn Lys Lys Phe  
260 265 270  
His Ser Phe Lys Lys Ile Val Arg Ser Leu Gly Tyr Gly Glu Glu Asp  
275 280 285  
Leu Pro Leu Val Ser Tyr Gln Ser Val Ser Lys Gly Tyr Tyr Gly Glu  
290 295 300  
Cys Gly Lys Arg Gly Gly Tyr Phe Glu Ile Thr Gly Phe Ser Ala Pro  
305 310 315 320  
Val Arg Glu Gln Ile Tyr Lys Ile Ala Ser Val Asn Leu Cys Ser Asn  
325 330 335  
Ile Thr Gly Gln Ile Leu Ala Ser Leu Val Met Asn Pro Pro Lys Ala

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Ser	Asp	Glu	Ser	Tyr	Ala	Ser	Tyr	Lys	Ala	Glu	Lys	Asp	Gly	Ile	Leu		
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Leu	Glu	Gly	Ile	Thr	Cys	Asn	Glu	Ala	Glu	Gly	Ala	Met	Tyr	Val	Phe		
385					390					395					400		
Pro	Gln	Ile	Cys	Leu	Pro	Gln	Lys	Ala	Ile	Glu	Ala	Ala	Lys	Ala	Ala		
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Asn	Lys	Ala	Pro	Asp	Ala	Phe	Tyr	Ala	Leu	Arg	Leu	Leu	Glu	Ser	Thr		
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Gly	Ile	Val	Val	Val	Pro	Gly	Ser	Gly	Phe	Gly	Gln	Val	Pro	Gly	Thr		
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Trp	His	Phe	Arg	Cys	Thr	Ile	Leu	Pro	Gln	Glu	Asp	Lys	Ile	Pro	Ala		
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Val	Ile	Ser	Arg	Phe	Thr	Val	Phe	His	Glu	Ala	Phe	Met	Ser	Glu	Tyr		
465					470					475					480		
Arg	Asp																